Cacnb2 Cas9-KO Strategy

Designer: Daohua Xu

Reviewer: Huimin Su

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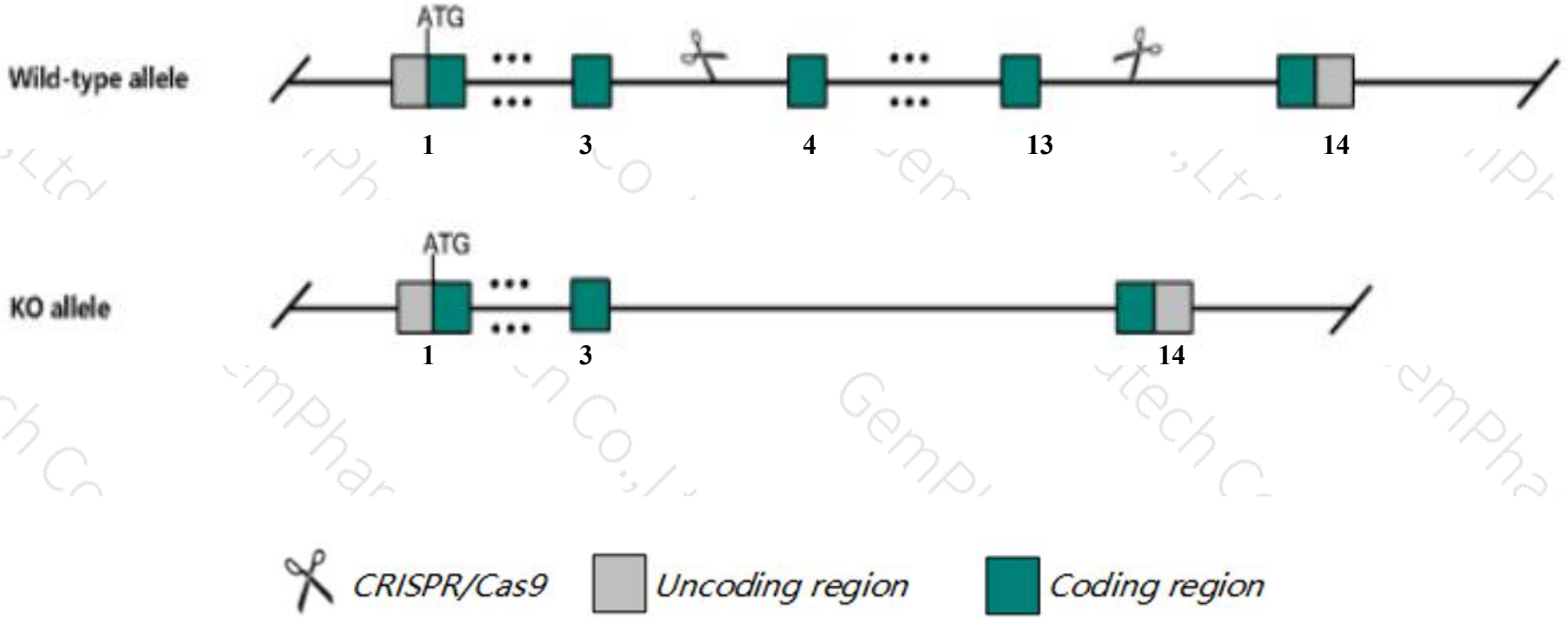
Project Overview

Project Name	***Cacnb2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cacnb2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cacnb2* gene has 16 transcripts. According to the structure of *Cacnb2* gene, exon4-exon13 of *Cacnb2-203* (ENSMUST00000114723.8) transcript is recommended as the knockout region.The region contains 1158bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cacnb2* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,mice homozygous for a null allele exhibit lethality at e10.5 with growth retardation, abnormal yolk vasculature and abnormal cardiac development and function.
- The KO region contains functional region of the *Gm37891* gene.Knockout the region may affect the function of *Gm37891* gene.
- The KO region deletes most of the coding sequence, but does not result in frameshift.
- The *Cacnb2* gene is located on the Chr2. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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Cacnb2 calcium channel, voltage-dependent, beta 2 subunit [Mus musculus (house mouse)]

Gene ID: 12296, updated on 20-Mar-2020

Summary

Official Symbol	Cacnb2 provided by MGI
Official Full Name	calcium channel, voltage-dependent, beta 2 subunit provided byMGI
Primary source	MGI:MGI:894644
See related	Ensembl:ENSMUSG00000057914
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW060387, CAB2, Cavbeta2, Cchb2
Expression	Broad expression in heart adult (RPKM 6.4), cerebellum adult (RPKM 5.3) and 18 other tissuesSee more
Orthologs	human all

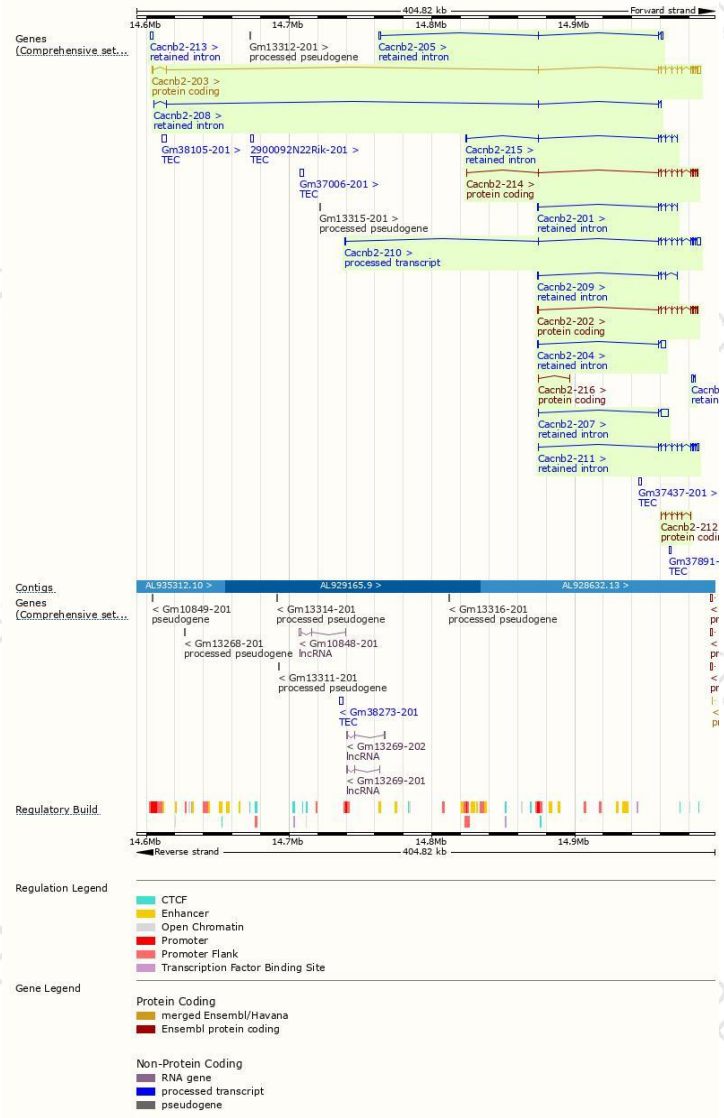
Transcript information（Ensembl）

The gene has 16 transcripts,all transcripts are shown below:

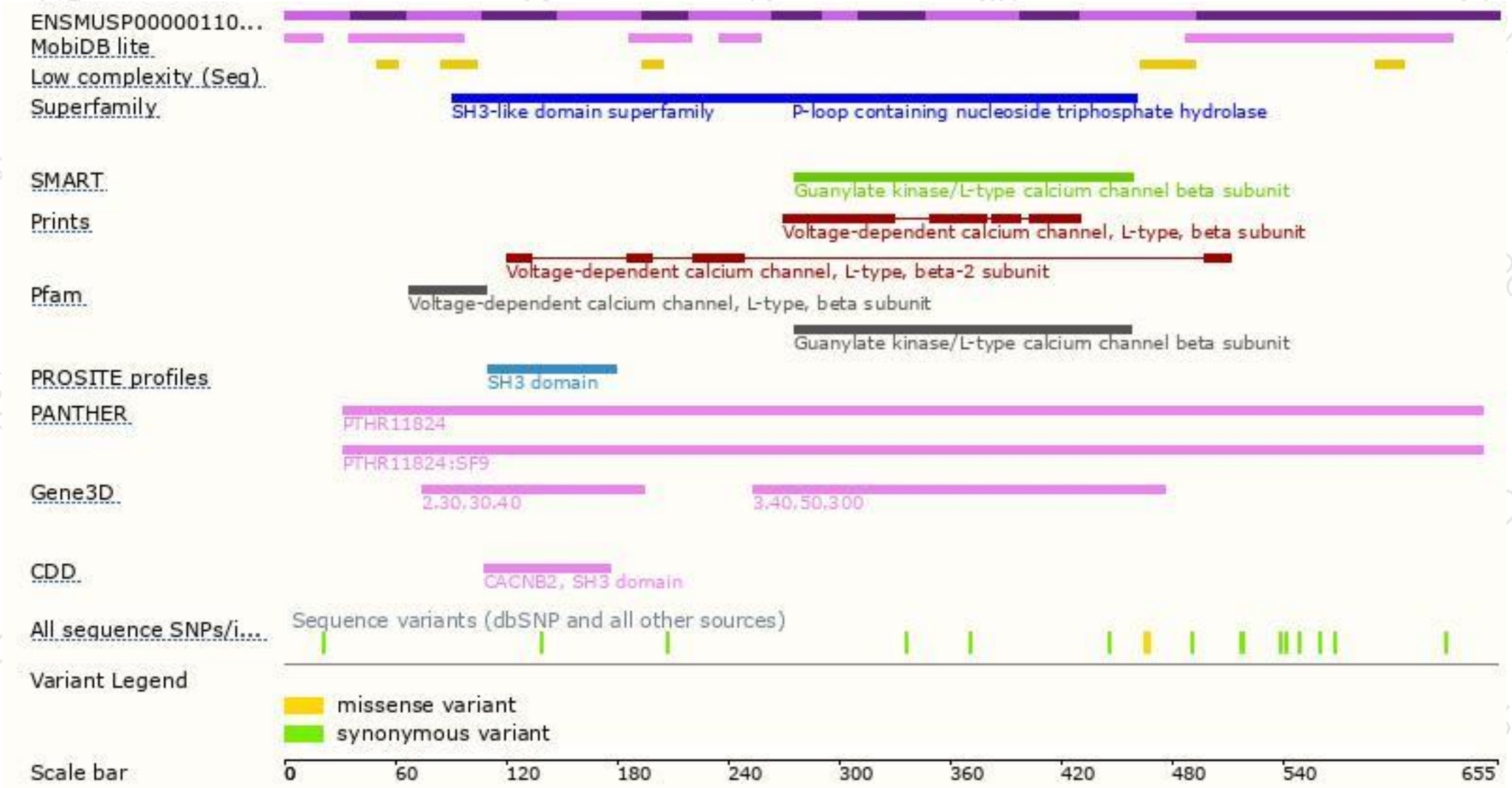
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cacnb2-203	ENSMUST00000114723.8	3945	655aa	Protein coding	CCDS15702	Q32MF3 Q8CC27	TSL:1 GENCODE basic
Cacnb2-202	ENSMUST00000114719.6	2117	611aa	Protein coding	CCDS84473	Q8CC27	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Cacnb2-214	ENSMUST00000193800.5	2117	605aa	Protein coding	CCDS79735	C7IVS7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Cacnb2-216	ENSMUST00000195841.1	503	72aa	Protein coding	-	A0A0A6YY52	TSL:3 GENCODE basic
Cacnb2-212	ENSMUST00000193522.1	430	143aa	Protein coding	-	A0A0A6YWX5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Cacnb2-210	ENSMUST00000193262.5	4146	No protein	Processed transcript	-	-	TSL:5
Cacnb2-207	ENSMUST00000148676.7	5030	No protein	Retained intron	-	-	TSL:2
Cacnb2-204	ENSMUST00000123719.6	3457	No protein	Retained intron	-	-	TSL:1
Cacnb2-211	ENSMUST00000193452.1	2802	No protein	Retained intron	-	-	TSL:5
Cacnb2-205	ENSMUST00000137746.7	2144	No protein	Retained intron	-	-	TSL:1
Cacnb2-213	ENSMUST00000193730.1	1526	No protein	Retained intron	-	-	TSL:NA
Cacnb2-215	ENSMUST00000194921.5	1052	No protein	Retained intron	-	-	TSL:5
Cacnb2-209	ENSMUST00000191903.5	942	No protein	Retained intron	-	-	TSL:5
Cacnb2-206	ENSMUST00000144423.1	935	No protein	Retained intron	-	-	TSL:3
Cacnb2-201	ENSMUST00000114718.7	867	No protein	Retained intron	-	-	TSL:5
Cacnb2-208	ENSMUST00000156027.7	669	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Cacnb2-203* transcript,the transcription is shown below:

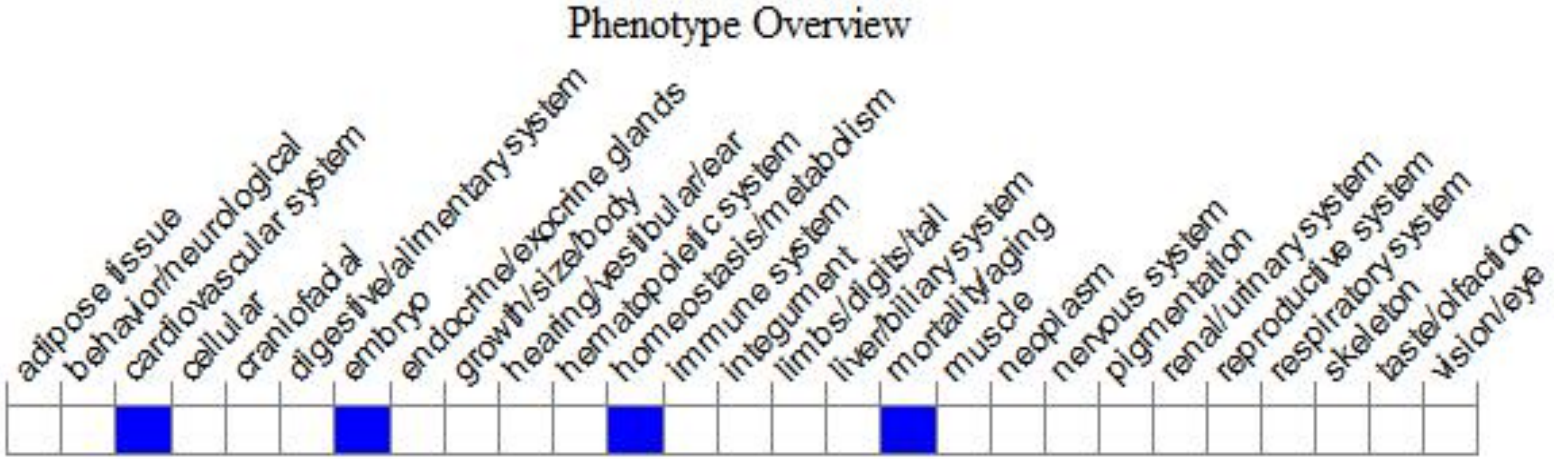
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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If you have any questions, you are welcome to inquire.

Tel: 400-9660890

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